

Table S1: Summary of isolated phages with their respective isolation host and source of isolation.

Phage ID	Isolation host serotype	Isolation source	GPS coordinate
PRF-SP1	<i>Salmonella</i> Paratyphi A	Dry sandy soil	5°27'43.2"N 100°11'24.0"E
PRF-SP2	<i>Salmonella</i> Paratyphi A	Wet soil	5°26'56.1"N 100°11'42.8"E
PRF-SP3	<i>Salmonella</i> Paratyphi A	Pond Water	5°26'49.3"N 100°11'39.5"E
PRF-SP4	<i>Salmonella</i> Paratyphi B	Wet soil	5°26'56.1"N 100°11'42.8"E
PRF-SP5	<i>Salmonella</i> Paratyphi B	Pond Water	5°26'49.3"N 100°11'39.5"E
PRF-SP6	<i>Salmonella</i> Paratyphi B	Dry sandy soil	5°27'43.2"N 100°11'24.0"E
PRF-SP7	<i>Salmonella</i> Paratyphi C	Dry sandy soil	5°27'43.2"N 100°11'24.0"E
PRF-SP8	<i>Salmonella</i> Paratyphi C	Wet soil	5°26'56.1"N 100°11'42.8"E
PRF-SP9	<i>Salmonella</i> Paratyphi C	Pond Water	5°26'49.3"N 100°11'39.5"E
PRF-SP10	<i>Salmonella</i> Typhi	Dry sandy soil	5°27'43.2"N 100°11'24.0"E
PRF-SP11	<i>Salmonella</i> Typhi	Wet soil	5°26'56.1"N 100°11'42.8"E
PRF-SP12	<i>Salmonella</i> Enteritidis	Wet soil	5°26'56.1"N 100°11'42.8"E
PRF-SP13	<i>Salmonella</i> Enteritidis	Pond Water	5°26'49.3"N 100°11'39.5"E

Table S2: Morphological features of phages PRF-SP1, PRF-SP3, PRF-SP4 and PRF-SP5

Phage ID	Head Diameter (nm)	Tail Length (nm)
PRF-SP1	58 ± 2.5	23 ± 2.2
PRF-SP3	50 ± 2.1	15 ± 2.2
PRF-SP4	75 ± 2.4	18 ± 2.1
PRF-SP5	76 ± 2.2	10 ± 2.5

Table S3: Summary of phage genome details

Phage	Genome size (bp)	Number of Coding Sequence	GC content (%)
PRF-SP1	39,732	49	50.26
PRF-SP3	39,849	49	50.28
PRF-SP4	39,829	49	50.24
PRF-SP5	39,849	49	50.28

Table S4: Single Nucleotide Polymorphism analysis between the newly isolated phages with each other. A: PRF-SP1(Ref) vs PRF-SP4(Qry); B: PRF-SP1(Ref) vs PRF-SP3(Qry); C: PRF-SP1(Ref) vs PRF-SP5(Qry); D: PRF-SP3(Ref) vs PRF-SP5(Qry); E: PRF-SP4(Ref) vs PRF-SP5(Qry); F: PRF-SP3(Ref) vs PRF-SP4(Qry). **Ref = Reference genome; Qry= Query

A.	Phage	Position	Change	Effect	Amino acid change	Predicted function
	PRF-SP1(REF) vs PRF-SP4 (QRY)	10893	C -> T	Non- Synonymous	P 83 L	Hypothetical protein
		25828	A -> T	Non- Synonymous	T 706 S	Tail tubular protein gp12
		35041	C -> T	Non- Synonymous	A 529 V	Tail spike protein
		35089	C -> A	Non- Synonymous	P 545 Q	
		35103	T -> G	Non- Synonymous	S 550 A	
B.	PRF-SP1(REF) vs PRF-SP3(QRY)	35373	T -> G	Non- Synonymous	S 640 A	
C.	Phage	Position	Change	Effect	Amino acid change	Predicted function
	PRF-SP1 (REF) vs PRF-SP5 (QRY)	25828	A -> G	Non- Synonymous	T 706 S	Tail tubular protein gp12
		35041	C -> T	Non- Synonymous	A 529 V	Tail spike protein
		35089	C -> A	Non- Synonymous	P 545 Q	
		35103	T -> G	Non- Synonymous	S 550 A	

D.

Phage	Position	Change	Effect	Amino acid change	Predicted function
PRF-SP3 (REF) vs PRF-SP5 (QRY)	26009	T -> C	Non- Synonymous	Y 727 C	Tail tubular protein gp12

E.

Phage	Position	Change	Effect	Amino acid change	Predicted function
PRF-SP4 (REF) vs PRF-SP5 (QRY)	10990	T -> C	Non- Synonymous	P 83 L	Hypothetical protein
	33411	A -> G	Synonymous	-	Peptidoglycan hydrolase
	3063	G -> T	Synonymous	-	T7 RNA Polymerase
	35470	T -> G	Non- Synonymous	A 640 S	Tail spike protein

F.

Phage	Position	Change	Effect	Amino acid change	Predicted function
PRF-SP3 (REF) vs PRF-SP4 (QRY)	35490	A -> C	Non- Synonymous	S 640 A	Tail spike protein
	11010	G -> A	Non- Synonymous	P 83 L	Hypothetical protein